IN THE SPECIFICATION:

Please replace paragraph no. [0004] with the following paragraph. The amendments to paragraph no. [0004] are indicated by strikethrough and underlining.

[0004] Although the etiology of breast cancer has not been elucidated, it is hypothesized to evolve from normal epithelium through certain non-malignant proliferative diseases to carcinoma in situ (Stage 0), either ductal or lobule, to primary invasive cancer (Stages I-IV) and finally, to metastatic (Stages III-IV). At some point in the progression from normal tissue to malignancy, tumor initiation occurs. Tumor initiation and the early stages of progression, do not necessarily render a cell malignant. The cells may, in fact, appear histologically normal even after initiation. A method of detecting mammary cells that have undergone tumor initiation but that are not yet neoplastic would be very useful in determining the most effective ~~the~~ course of disease treatment.

Please replace paragraph no. [0026] with the following paragraph. The amendments to paragraph no. [0026] are indicated by strikethrough and underlining.

[0026] The present inventors have correlated LOH at chromosomal locus 3p24.3 in morphologically normal cells with an increased risk for the development of cancer in those cells. ~~Additional~~ Additionally, they have found that the LOH at 3p24.3 is correlated with a decrease in expression of the thyroid hormone receptor β1 gene in these cells. This decrease in expression is not due entirely to the deletion of the gene as one copy of the gene is still present on the remaining allele. Rather, the decrease in expression can be attributed to an increase in methylation of the *TRβ1* promoter. Therefore, analysis of the methylation state of the chromosome in the region of the *TRβ1* promoter or analysis of the expression of the *TRβ1* gene, can provide a similar kind of predictive information as analysis of the LOH at 3p24.3.

Please replace paragraph no. [0030] with the following paragraph. The amendments to paragraph no. [0030] are indicated by strikethrough and underlining.

[0030] Techniques for analysis of the level of any particular transcript in a cell are well known in the art and include, for example, Northern blot analysis and RT-PCR (See, for example, Sambrook et al. Molecular Cloning: A Laboratory Manual, 2nd Ed. Cold Spring Harbor Laboratories Press 1989; Mocharla et al. Gene 1990 93:271). For analysis of mRNA transcript levels for the *TRβ1* gene, a particularly useful technique is RT-PCR. Primers that are useful in this regard include *TRβ-F* and *TRβ-R*. Other useful primers and probes may be designed based on the sequence of the *TRβ1* gene and mRNA (Weinberger et al. Nature (1986) 324:641; Human Genome Project Working Draft ~~at http://genome.ucsc.edu~~) by methods that are well known. Analysis of the level of the *TRβ1* protein may be carried out by any convenient method; for example, Western blot analysis and ELISA assay (Sambrook et al. 1989). Immunoassays using anti-*TRβ1* antibodies, for example, monoclonal antibody J51, are particularly useful in the method of the present invention. Analysis of the expression of the *TRβ1* gene in the target cells will include the comparison to *TRβ1* gene expression in a control cell sample. One of ordinary skill in the art is competent to select the appropriate control cell sample. The control cell sample will generally include cells of the same type from the same tissue as the target cells but will be from a cancer free individual or from a cancer free region of the patient. Standard control cell samples can be developed for use with different target cell samples. Moreover, standard values for *TRβ1* expression levels can be developed from the control cell samples, for both mRNA and protein analysis, such that actual measurement of the expression in the control cell sample need not be carried out with each analysis, but rather the target cell samples can be compared to a standard value for protein or mRNA developed from the control cell samples.